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Page 1 of 8



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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/079,384

DATE: 07/29/2002 8:6
TIME: 13:32:10

Input Set : A:\Seq listing 9409-2135.txt
Output Set: N:\CRF3\07292002\J079384.raw

3 <110> APPLICANT: Communi, Didier
5 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED
RECEPTORS

7 <130> FILE REFERENCE: 9409/2132
9 <140> CURRENT APPLICATION NUMBER: US 10/079,384
10 <141> CURRENT FILING DATE: 2002-02-20
12 <150> PRIOR APPLICATION NUMBER: US 09/885,453
13 <151> PRIOR FILING DATE: 2001-06-20
15 <160> NUMBER OF SEQ ID NOS: 50
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1356
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (1)..(1356)
27 <223> OTHER INFORMATION:
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32 1 5 10 15
34 ggg agg gtc cct caa acc cca ggt ccc tct act gcc agt ggg gtc ccg 96
35 Gly Arg Val Pro Gln Thr Pro Gly Pro Ser Thr Ala Ser Gly Val Pro
36 20 25 30
38 gaq gtg ggg cta cgg gat gtt gct tcg gaa tct gtg gcc ctc ttc ttc 144
39 Glu Val Gly Leu Arg Asp Val Ala Ser Glu Ser Val Ala Leu Phe Phe
40 35 40 45
42 atq ctc ctg ctg gac ttg act gct gtg gct ggc aat gcc gct gtg atg 192
43 Met Leu Leu Asp Leu Thr Ala Val Ala Gly Asn Ala Ala Val Met
44 50 55 60
46 gcc gtg atc gcc aag acg cct gcc ctc cga aaa ttt gtc ttc gtc ttc 240
47 Ala Val Ile Ala Lys Thr Pro Ala Leu Arg Lys Phe Val Phe Val Phe
48 65 70 75 80
50 cac ctc tgc ctg gtg gac ctg ctg gct gcc ctg acc ctc atg ccc ctg 288
51 His Leu Cys Leu Val Asp Leu Leu Ala Ala Leu Thr Leu Met Pro Leu
52 85 90 95
54 gcc atg ctc tcc agc tct gcc ctc ttt gac cac gcc ctc ttt ggg gag 336
55 Ala Met Leu Ser Ser Ala Leu Phe Asp His Ala Leu Phe Gly Glu
56 100 105 110
58 gtg gcc tgc cgc ctc tac ttg ttt ctg agc gtg tgc ttt gtc agc ctg 384
59 Val Ala Cys Arg Leu Tyr Leu Phe Leu Ser Val Cys Phe Val Ser Leu
60 115 120 125
62 gcc atc ctc tgc gtg tca gcc atc aat gtg gag cgc tac tat tac gta 432

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/079,384

DATE: 07/29/2002
TIME: 13:32:11

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Output Set: N:\CRF3\07292002\J079384.raw

63	Ala	Ile	Leu	Ser	Val	Ser	Ala	Ile	Asn	Val	Glu	Arg	Tyr	Tyr	Tyr	Val	
64	130						135				140						
66	gtc	cac	ccc	atg	cgc	tac	gag	gtg	cgc	atg	acg	ctg	ggg	ctg	gtg	gcc	480
67	Val	His	Pro	Met	Arg	Tyr	Glu	Val	Arg	Met	Thr	Leu	Gly	Leu	Val	Ala	
68	145						150				155				160		
70	tct	gtg	ctg	gtg	gtt	gtg	tgg	gtg	aag	gcc	ttg	gcc	atg	gct	tct	gtg	528
71	Ser	Val	Leu	Val	Gly	Val	Trp	Val	Lys	Ala	Leu	Ala	Met	Ala	Ser	Val	
72							165				170				175		
74	cca	gtg	ttg	gga	agg	gtc	tcc	tgg	gag	gaa	gga	gct	ccc	agt	gtc	ccc	576
75	Pro	Val	Leu	Gly	Arg	Val	Ser	Trp	Glu	Glu	Gly	Ala	Pro	Ser	Val	Pro	
76							180				185				190		
78	cca	ggc	tgt	tca	ctc	cag	tgg	agc	cac	agt	gcc	tac	tgc	cag	ctt	ttt	624
79	Pro	Gly	Cys	Ser	Leu	Gln	Trp	Ser	His	Ser	Ala	Tyr	Cys	Gln	Leu	Phe	
80							195				200				205		
82	gtg	gtg	gtc	ttt	gct	gtc	ctt	tac	ttt	ctg	ttg	ccc	ctg	ctc	ctc	ata	672
83	Val	Val	Val	Phe	Ala	Val	Leu	Tyr	Phe	Leu	Leu	Pro	Leu	Leu	Leu	Ile	
84							210				215				220		
86	ctt	gtg	gtc	tac	tgc	agc	atg	ttc	cga	gtg	gcc	cgc	gtg	gct	gcc	atg	720
87	Leu	Val	Val	Tyr	Cys	Ser	Met	Phe	Arg	Val	Ala	Arg	Val	Ala	Ala	Met	
88							225				230				235	240	
90	cag	cac	ggg	ccg	ctg	ccc	acg	tgg	atg	gag	aca	ccc	cgg	caa	cgc	tcc	768
91	Gln	His	Gly	Pro	Leu	Pro	Thr	Trp	Met	Glu	Thr	Pro	Arg	Gln	Arg	Ser	
92							245				250				255		
94	gaa	tct	ctc	agc	agc	cgc	tcc	acg	atg	gtc	acc	agc	tgc	ggg	gcc	ccc	816
95	Glu	Ser	Leu	Ser	Arg	Ser	Thr	Met	Val	Thr	Ser	Ser	Gly	Ala	Pro		
96							260				265				270		
98	cag	acc	acc	cca	cac	ccg	acg	ttt	ggg	gga	ggg	aaa	gca	gca	gtg	gtt	864
99	Gln	Thr	Thr	Pro	His	Arg	Thr	Phe	Gly	Gly	Gly	Lys	Ala	Ala	Val	Val	
100							275				280				285		
102	ctc	ctg	gct	gtg	ggg	gga	cag	tcc	ctg	ctc	tgt	tgg	ccc	tac	tcc	912	
103	Leu	Leu	Ala	Val	Gly	Gly	Gln	Phe	Leu	Leu	Cys	Trp	Leu	Pro	Tyr	Phe	
104							290				295				300		
106	tct	ttc	cac	ctc	tat	gtt	gcc	ctg	agt	gtc	cag	ccc	att	tca	act	ggg	960
107	Ser	Phe	His	Leu	Tyr	Val	Ala	Leu	Ser	Ala	Gln	Pro	Ile	Ser	Thr	Gly	
108							305				310				315	320	
110	cag	gtg	gag	agt	gtg	gtc	acc	tgg	att	ggc	tac	ttt	tgc	tcc	act	tcc	1008
111	Gln	Val	Glu	Ser	Val	Val	Thr	Trp	Ile	Gly	Tyr	Phe	Cys	Phe	Thr	Ser	
112							325				330				335		
114	aac	cct	ttc	ttc	tat	gga	tgt	ctc	aac	ccg	cag	atc	ccg	ggg	gag	ctc	1056
115	Asn	Pro	Phe	Phe	Tyr	Gly	Cys	Leu	Asn	Arg	Gln	Ile	Arg	Gly	Glu	Leu	
116							340				345				350		
118	agc	aag	cag	ttt	gtc	tgc	ttc	tcc	aag	cca	gct	cca	gag	gag	gag	ctg	1104
119	Ser	Lys	Gln	Phe	Val	Cys	Phe	Phe	Lys	Pro	Ala	Pro	Glu	Glu	Glu	Leu	
120							355				360				365		
122	agg	ctg	cct	agc	ccg	gag	ggc	tcc	att	gag	gag	aac	ttc	ctg	cag	tcc	1152
123	Arg	Leu	Pro	Ser	Arg	Glu	Gly	Ser	Ile	Glu	Glu	Asn	Phe	Leu	Gln	Phe	
124							370				375				380		
126	ctt	cag	ggg	act	ggc	tgt	cct	tct	gag	tcc	tgg	gtt	tcc	cga	ccc	cta	1200
127	Leu	Gln	Gly	Thr	Gly	Cys	Pro	Ser	Glu	Ser	Trp	Val	Ser	Arg	Pro	Leu	

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/079,384

DATE: 07/29/2002
TIME: 13:32:11

Input Set : A:\Seq listing 9409-2135.txt
Output Set: N:\CRF3\07292002\J079384.raw

128	385	390	395	400													
130	ccc	agg	ccg	ttt	1248												
131	Pro	Ser	Pro	Lys	Gln	Glu	Pro	Pro	Ala	Val	Asp	Phe	Arg	Ile	Pro	Gly	
132					405					410					415		
134	cag	ata	gct	gag	acc	tct	gag	ttc	ctg	gag	cag	caa	ctc	acc	agc		1296
135	Gln	Ile	Ala	Glu	Glu	Thr	Ser	Glu	Phe	Leu	Glu	Gln	Gln	Leu	Thr	Ser	
136					420					425					430		
138	gac	atc	atc	atg	tca	gac	agc	tac	ctc	cgt	cct	gcc	gcc	tca	ccc	cgg	1344
139	Asp	Ile	Ile	Met	Ser	Asp	Ser	Tyr	Leu	Arg	Pro	Ala	Ala	Ser	Pro	Arg	
140					435					440					445		
142	ctg	gag	tca	tga												1356	
143	Leu	Glu	Ser														
144		450															
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148	<211>	LENGTH:	451														
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155	1				5				10						15		
158	Gly	Arg	Val	Pro	Gln	Thr	Pro	Gly	Pro	Ser	Thr	Ala	Ser	Gly	Val	Pro	
159					20				25						30		
162	Glu	Val	Gly	Leu	Arg	Asp	Val	Ala	Ser	Glu	Ser	Val	Ala	Leu	Phe	Phe	
163					35				40						45		
166	Met	Leu	Leu	Leu	Asp	Leu	Thr	Ala	Val	Ala	Gly	Asn	Ala	Ala	Val	Met	
167					50				55						60		
170	Ala	Val	Ile	Ala	Lys	Thr	Pro	Ala	Leu	Arg	Lys	Phe	Val	Phe	Val	Phe	
171	65				70				75						80		
174	His	Leu	Cys	Leu	Val	Asp	Leu	Ala	Ala	Leu	Thr	Leu	Met	Pro	Leu		
175					85				90						95		
178	Ala	Met	Leu	Ser	Ser	Ser	Ala	Leu	Phe	Asp	His	Ala	Leu	Phe	Gly	Glu	
179					100				105						110		
182	Val	Ala	Cys	Arg	Leu	Tyr	Leu	Phe	Leu	Ser	Val	Cys	Phe	Val	Ser	Leu	
183					115				120						125		
186	Ala	Ile	Leu	Ser	Val	Ser	Ala	Ile	Asn	Val	Glu	Arg	Tyr	Tyr	Tyr	Val	
187					130				135						140		
190	Val	His	Pro	Met	Arg	Tyr	Glu	Val	Arg	Met	Thr	Leu	Gly	Leu	Val	Ala	
191	145				150				155						160		
194	Ser	Val	Leu	Val	Gly	Val	Trp	Val	Lys	Ala	Leu	Ala	Met	Ala	Ser	Val	
195					165				170						175		
198	Pro	Val	Leu	Gly	Arg	Val	Ser	Trp	Glu	Glu	Gly	Ala	Pro	Ser	Val	Pro	
199					180				185						190		
202	Pro	Gly	Cys	Ser	Leu	Gln	Trp	Ser	His	Ser	Ala	Tyr	Cys	Gln	Leu	Phe	
203					195				200						205		
206	Val	Val	Val	Phe	Ala	Val	Leu	Tyr	Phe	Leu	Leu	Pro	Leu	Leu	Leu	Ile	
207					210				215						220		
210	Ieu	Val	Val	Tyr	Cys	Ser	Met	Phe	Arg	Val	Ala	Arg	Val	Ala	Ala	Met	
211	225				230				235						240		
214	Gln	His	Gly	Pro	Leu	Pro	Thr	Trp	Met	Glu	Thr	Pro	Arg	Gln	Arg	Ser	

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DATE: 07/29/2002

PATENT APPLICATION: US/10/079,384

TIME: 13:32:11

Input Set : A:\Seq listing 9409-2135.txt

Output Set: N:\CRF3\07292002\J079384.raw

215	245	250	255	
218	Glu Ser Leu Ser Ser Arg Ser Thr Met Val Thr Ser Ser Gly Ala Pro			
219	260	265	270	
222	Gln Thr Thr Pro His Arg Thr Phe Gly Gly Gly Lys Ala Ala Val Val			
223	275	280	285	
226	Leu Leu Ala Val Gly Gly Gln Phe Leu Leu Cys Trp Leu Pro Tyr Phe			
227	290	295	300	
230	Ser Phe His Leu Tyr Val Ala Leu Ser Ala Gln Pro Ile Ser Thr Gly			
231	305	310	315	320
234	Gln Val Glu Ser Val Val Thr Trp Ile Gly Tyr Phe Cys Phe Thr Ser			
235	325	330	335	
238	Asn Pro Phe Phe Tyr Gly Cys Leu Asn Arg Gln Ile Arg Gly Glu Leu			
239	340	345	350	
242	Ser Lys Gln Phe Val Cys Phe Phe Lys Pro Ala Pro Glu Glu Glu Leu			
243	355	360	365	
246	Arg Leu Pro Ser Arg Glu Gly Ser Ile Glu Glu Asn Phe Leu Gln Phe			
247	370	375	380	
250	Leu Gln Gly Thr Gly Cys Pro Ser Glu Ser Trp Val Ser Arg Pro Leu			
251	385	390	395	400
254	Pro Ser Pro Lys Gln Glu Pro Pro Ala Val Asp Phe Arg Ile Pro Gly			
255	405	410	415	
258	Gln Ile Ala Glu Glu Thr Ser Glu Phe Leu Glu Gln Gln Leu Thr Ser			
259	420	425	430	
262	Asp Ile Ile Met Ser Asp Ser Tyr Leu Arg Pro Ala Ala Ser Pro Arg			
263	435	440	445	
266	Leu Glu Ser			
267	450			
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271	<211> LENGTH 969			
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273	<213> ORGANISM: Homo sapiens			
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276	<221> NAME/KEY: CDS			
277	<222> LOCATION: (1)..(969)			
278	<223> OTHER INFORMATION:			
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283	1 5 10 15			
285	gga act gag qag act ctt tgc tac aag cag acc ttg agc ctc acg gtg		96	
286	Gly Thr Glu Glu Thr Leu Cys Tyr Lys Gln Thr Leu Ser Leu Thr Val			
287	20 25 30			
289	ctg acg tgc atc gtt tcc ctt gtc ggg ctg aca gga aac gca gtt gtg		144	
290	Leu Thr Cys Ile Val Ser Leu Val Gly Leu Thr Gly Asn Ala Val Val			
291	35 40 45			
293	ctc tgg ctc ctg ggc tgc cgc atg cgc agg aac gcc ttc tcc atc tac		192	
294	Leu Trp Leu Leu Gly Cys Arg Met Arg Arg Asn Ala Phe Ser Ile Tyr			
295	50 55 60			
297	atc ctc aac ttg gcc gca gac ttc ctc ttc agc ggc cgc ctt		240	

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/079,384

DATE 07/29/2002
TIME: 13 32:11

Input Set : A:\Seq listing 9409-2135.txt
Output Set: N:\CRF3\07292002\J079384.raw

298	Ile	Leu	Asn	Leu	Ala	Ala	Asp	Phe	Leu	Phe	Leu	Ser	Gly	Arg	Leu			
299	65				70			75				80						
301	ata	tat	tcc	ctg	tta	agc	ttc	atc	agt	atc	ccc	cat	acc	atc	tct	aaa	288	
302	Ile	Tyr	Ser	Leu	Leu	Ser	Phe	Ile	Ser	Ile	Pro	His	Thr	Ile	Ser	Lys		
303					85				90			95						
305	atc	ctc	tat	cct	gtg	atg	atg	ttt	tcc	tac	ttt	gca	ggc	ctg	agc	ttt	336	
306	Ile	Leu	Tyr	Pro	Val	Met	Met	Phe	Ser	Tyr	Phe	Ala	Gly	Leu	Ser	Phe		
307					100				105			110						
309	ctg	agt	gcc	gtg	agc	acc	gag	cgc	tgc	ctg	tcc	gtc	ctg	tgg	ccc	atc	384	
310	Leu	Ser	Ala	Val	Ser	Thr	Glu	Arg	Cys	Leu	Ser	Val	Leu	Trp	Pro	Ile		
311					115			120			125							
313	tgg	tac	cgc	tgc	cac	cgc	ccc	aca	cac	ctg	tca	gcg	gtg	gtg	tgt	gtc	432	
314	Trp	Tyr	Arg	Cys	His	Arg	Pro	Thr	His	Leu	Ser	Ala	Val	Val	Cys	Val		
315					130			135			140							
317	ctg	ctc	tgg	gcc	ctg	tcc	ctg	ctg	cg	agc	atc	ctg	gag	tgg	atg	tta	480	
318	Leu	Leu	Trp	Ala	Leu	Ser	Leu	Leu	Arg	Ser	Ile	Leu	Glu	Trp	Met	Leu		
319	145				150				155			160						
321	tgt	ggc	ttc	ctg	ttc	agt	gg	gt	gt	at	tct	gt	ttg	tgt	caa	aca	528	
322	Cys	Gly	Phe	Leu	Phe	Ser	Gly	Ala	Asp	Ser	Ala	Trp	Cys	Gln	Thr	Ser		
323					165			170			175							
325	gat	ttc	atc	aca	gtc	g	ttg	ctg	att	ttt	tta	tgt	gt	tt	ctc	tgt	576	
326	Asp	Phe	Ile	Thr	Val	Ala	Trp	Leu	Ile	Phe	Leu	Cys	Val	Val	Leu	Cys		
327					180			185			190							
329	ggg	tcc	agc	ctg	gtc	ctg	atc	agg	att	ctc	tgt	gga	tcc	cg	aag		624	
330	Gly	Ser	Ser	Leu	Val	Leu	Leu	Ile	Arg	Ile	Leu	Cys	Gly	Ser	Arg	Lys		
331					195			200			205							
333	ata	ccg	ctg	acc	agg	ctg	tac	gtg	acc	atc	ctg	ctc	aca	gta	ctg	gtc	672	
334	Ile	Pro	Leu	Thr	Arg	Leu	Tyr	Val	Thr	Ile	Leu	Leu	Thr	Val	Leu	Val		
335					210			215			220							
337	tcc	ctc	ctc	tgt	ggc	ctg	ccc	ttt	ggc	att	cag	ttt	tcc	cta	ttt	tta	720	
338	Phe	Leu	Leu	Cys	Gly	Leu	Pro	Phe	Gly	Ile	Gln	Phe	Phe	Leu	Phe	Leu		
339	225				230				235			240						
341	tgg	atc	cac	gtg	gac	agg	gaa	gtc	tta	ttt	tgt	cat	gtt	cat	cta	gtt	768	
342	Trp	Ile	His	Val	Asp	Arg	Glu	Val	Leu	Phe	Cys	His	Val	His	Leu	Val		
343					245			250			255							
345	tct	att	ttc	ctg	tcc	gct	ctt	aac	agc	agt	gcc	aac	ccc	atc	att	tac		
346	Ser	Ile	Phe	Leu	Ser	Ala	Leu	Asn	Ser	Ser	Ala	Asn	Pro	Ile	Ile	Tyr		
347					260			265			270							
349	tcc	ttc	gtg	ggc	tcc	ttt	agg	cag	cgt	caa	aat	agg	cag	aac	ctg	aag	864	
350	Phe	Phe	Val	Gly	Ser	Phe	Arg	Glu	Val	Leu	Phe	Cys	His	Val	His	Leu	Lys	
351					275			280			285							
353	ctg	gtt	ctc	cag	agg	gct	ctg	cag	gac	g	tct	gag	gt	gat	gaa	ggt	912	
354	Leu	Val	Leu	Gln	Arg	Ala	Leu	Gln	Asp	Ala	Ser	Glu	Val	Asp	Glu	Gly		
355					290			295			300							
357	gga	ggg	cag	ctt	cct	gag	gaa	atc	ctg	gag	tcg	gga	agc	aga	ttg		960	
358	Gly	Gly	Gln	Leu	Pro	Glu	Glu	Ile	Leu	Glu	Leu	Ser	Gly	Ser	Arg	Leu		
359	305				310				315			320						
361	gag	cag	cag	tga												964		
362	Glu	Gln																

RAW SEQUENCE LISTING ERROR SUMMARY DATE 07/29/2002
PATENT APPLICATION: US/10/079,384 TIME 13:32:12

Input Set : A:\Seq listing 9409-2135.txt
Output Set: N:\CRF3\07292002\J079384.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq# : 35; Xaa Pos. 1,4
Seq# : 36; Xaa Pos. 1,4,8

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/079,384

DATE: 07/29/2002

TIME: 13:32:12

Input Set : A:\Seq listing 9409-2135.txt
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L:2968 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:0
L:3008 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0